RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/533,361_

Source: _PCT/10_

Date Processed by STIC: _5/12/05_

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PCT

RAW SEQUENCE LISTING   DATE: 05/12/2005
PATENT APPLICATION: US/10/533,361   TIME: 08:02:34

          Input Set : A:\44-05sequence listing.txt
          Output Set: N:\CRF4\05122005\J533361.raw

     3 <110> APPLICANT: BURTON, KERRY
     4   CHALLEN, MICHAEL
     5   ELLIOTT, TIMOTHY
     6   SREENIVASAPRASAD, SURAPAREDDY
     7   EASTWOOD, DANIEL
     8   MOLLOY, SHANNON
    10 <120> TITLE OF INVENTION: SELECTIVE EXPRESSION IN FILAMENTOUS FUNGI
    12 <130> FILE REFERENCE: 44-05
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/533,361
C--> 14 <141> CURRENT FILING DATE: 2005-04-29
    14 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/004716
    15 <151> PRIOR FILING DATE: 2003-10-31
    17 <150> PRIOR APPLICATION NUMBER: UK 0225390.4
    18 <151> PRIOR FILING DATE: 2002-10-31
    20 <160> NUMBER OF SEQ ID NOS: 37
    22 <170> SOFTWARE: PatentIn version 3.1
    24 <210> SEQ ID NO: 1
    25 <211> LENGTH: 1736
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Agaricus bisporus
    29 <220> FEATURE:
    30 <221> NAME/KEY: CDS
    31 <222> LOCATION: (19)..(1674)
    32 <223> OTHER INFORMATION:
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    36 ggctgagctc tattcatc atg gcg tcg gaa cga cag att gaa gaa ctt ccc   51
    37   Met Ala Ser Glu Arg Gln Ile Glu Glu Leu Pro
    38   1   5   10
    40 agt tat aag tac gcc tat att ttg acg gca tcg gct tgc ttg gga agt   99
    41 Ser Tyr Lys Tyr Ala Tyr Ile Leu Thr Ala Ser Ala Cys Leu Gly Ser
    42   15   20   25
    44 gtg ttt cac ggg tgg gat gta ggc ctt ata gga ggc ata ctc tcg cta   147
    45 Val Phe His Gly Trp Asp Val Gly Leu Ile Gly Gly Ile Leu Ser Leu
    46   30   35   40
    48 cgg tca ttt caa gaa tat ctc ggg atc aat aca aaa aat gcc gtc aag   195
    49 Arg Ser Phe Gln Glu Tyr Leu Gly Ile Asn Thr Lys Asn Ala Val Lys
    50   45   50   55
    52 aaa gcg att cta gac gga aac atc atc tct gtg ctc caa gcc gga tgt   243
    53 Lys Ala Ile Leu Asp Gly Asn Ile Ile Ser Val Leu Gln Ala Gly Cys
    54 60   65   70   75
    56 ttt ttt ggc gcg ctt gga acc gga tat ctc tct agt cga ttc ggc cga   291
    57 Phe Phe Gly Ala Leu Gly Thr Gly Tyr Leu Ser Ser Arg Phe Gly Arg
    58   80   85   90

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60 aga ccc tgt ctt att gca tct ggt att gtg tat ata act ggc ggt ttg      339
61 Arg Pro Cys Leu Ile Ala Ser Gly Ile Val Tyr Ile Thr Gly Gly Leu
62          95                  100                 105
64 ctg caa tgc act gtc ggt ttg gga ccc tcg caa gct gct gct cta cac      387
65 Leu Gln Cys Thr Val Gly Leu Gly Pro Ser Gln Ala Ala Ala Leu His
66          110                 115                 120
68 gtg ttc tat att ggc agg ttc att tct ggt atc ggt gtt ggg atg gtg      435
69 Val Phe Tyr Ile Gly Arg Phe Ile Ser Gly Ile Gly Val Gly Met Val
70      125                 130                 135
72 tcc act ctc gtg cct ttg tat att tcg gag tgt gtc cct agg act ata      483
73 Ser Thr Leu Val Pro Leu Tyr Ile Ser Glu Cys Val Pro Arg Thr Ile
74 140                 145                 150                 155
76 cgc ggg cgc tgt act gga aca ctc caa ttt gcg act aac agt ggt ctg      531
77 Arg Gly Arg Cys Thr Gly Thr Leu Gln Phe Ala Thr Asn Ser Gly Leu
78          160                 165                 170
80 atg ctg ggc ttc tgg gtc aac tac agc gtg tcg aaa aac gtg ccc ttt      579
81 Met Leu Gly Phe Trp Val Asn Tyr Ser Val Ser Lys Asn Val Pro Phe
82          175                 180                 185
84 ggt gaa atg caa tgg cga att ccg tta att atc caa atg att ccg agc      627
85 Gly Glu Met Gln Trp Arg Ile Pro Leu Ile Ile Gln Met Ile Pro Ser
86          190                 195                 200
88 ctc ttg ttc atc ata gcc atg ttt ttc caa cca gaa tcg ccg aga tgg      675
89 Leu Leu Phe Ile Ile Ala Met Phe Phe Gln Pro Glu Ser Pro Arg Trp
90      205                 210                 215
92 ctt gtt gaa cac ggg aaa cac aag gaa gct gcg acg gta ctg gcg cgt      723
93 Leu Val Glu His Gly Lys His Lys Glu Ala Ala Thr Val Leu Ala Arg
94 220                 225                 230                 235
96 act ggc ggc aag gat gtt gat cat cct agt gtt gta cag aca ctg gag      771
97 Thr Gly Gly Lys Asp Val Asp His Pro Ser Val Val Gln Thr Leu Glu
98              240                 245                 250
100 gag atc aag caa gaa ttt gtg gcg agt aaa caa cca tcg ttt tta aag      819
101 Glu Ile Lys Gln Glu Phe Val Ala Ser Lys Gln Pro Ser Phe Leu Lys
102          255                 260                 265
104 cag att cgc ctg gtc ggt gaa tcg agg gct gtt gcc ctg agg tgc ttt      867
105 Gln Ile Arg Leu Val Gly Glu Ser Arg Ala Val Ala Leu Arg Cys Phe
106          270                 275                 280
108 ata cca ccg cta gtg atg ttc ttc cag cag tgg acg ggt aca aat gcc      915
109 Ile Pro Pro Leu Val Met Phe Phe Gln Gln Trp Thr Gly Thr Asn Ala
110      285                 290                 295
112 atc aac ctt tat agt ccc gaa gta ttc cgt cat ctt gga atc cat ggc      963
113 Ile Asn Leu Tyr Ser Pro Glu Val Phe Arg His Leu Gly Ile His Gly
114 300                 305                 310                 315
116 acc agc ggg gct ctc ttc gct act ggt gtt tat ggc gtg gtg aag gtt     1011
117 Thr Ser Gly Ala Leu Phe Ala Thr Gly Val Tyr Gly Val Val Lys Val
118                  320                 325                 330
120 gtt tca gtt gca ctt gcc ctc act ttt gct gtc gaa cgc ttt gga cgc     1059
121 Val Ser Val Ala Leu Ala Leu Thr Phe Ala Val Glu Arg Phe Gly Arg
122          335                 340                 345
124 aag aga ggg ttg att ttt ggt ggt atc ggc caa gca ctt atg atg ttt     1107
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                Input Set : A:\44-05sequence listing.txt
                Output Set: N:\CRF4\05122005\J533361.raw

125 Lys Arg Gly Leu Ile Phe Gly Gly Ile Gly Gln Ala Leu Met Met Phe
126         350                 355                 360
128 tgg ttg gga ggt tat agt gcc acc cac caa gac ggt act gtc agt cct   1155
129 Trp Leu Gly Gly Tyr Ser Ala Thr His Gln Asp Gly Thr Val Ser Pro
130     365                 370                 375
132 gcg agt cat gtt tcc att gtt gca ctc tac ttg tat ggt gca ttc ttc   1203
133 Ala Ser His Val Ser Ile Val Ala Leu Tyr Leu Tyr Gly Ala Phe Phe
134 380                 385                 390                 395
136 tcc atg gga tgg ggc cca tta cca tgg gtc gtc gct gga gag gtt gca   1251
137 Ser Met Gly Trp Gly Pro Leu Pro Trp Val Val Ala Gly Glu Val Ala
138             400                 405                 410
140 cct aac cat gtc cgc tcc ttc gcc ctc tcc atc gcc gtt gga act cat   1299
141 Pro Asn His Val Arg Ser Phe Ala Leu Ser Ile Ala Val Gly Thr His
142         415                 420                 425
144 tgg ctc ttc ggg ttt gtg ata tca aaa gtg acg cca att atg ttg gac   1347
145 Trp Leu Phe Gly Phe Val Ile Ser Lys Val Thr Pro Ile Met Leu Asp
146         430                 435                 440
148 cgt atc aaa tat ggc aca ttc cta ctc ttc gga ttc tgt tgc atg ata   1395
149 Arg Ile Lys Tyr Gly Thr Phe Leu Leu Phe Gly Phe Cys Cys Met Ile
150         445                 450                 455
152 gta gcg aca tgg gct tat ttc tgt cta cct gag aca agt ggg ttc gct   1443
153 Val Ala Thr Trp Ala Tyr Phe Cys Leu Pro Glu Thr Ser Gly Phe Ala
154 460                 465                 470                 475
156 ctg gag gac atc aaa tat ctg ttc gag cga gac gtc atc att cgt tca   1491
157 Leu Glu Asp Ile Lys Tyr Leu Phe Glu Arg Asp Val Ile Ile Arg Ser
158             480                 485                 490
160 ttg cag gac gct ccc ggt gga aaa ata ttc ttg ggg ggg agg cgt gtg   1539
161 Leu Gln Asp Ala Pro Gly Gly Lys Ile Phe Leu Gly Gly Arg Arg Val
162         495                 500                 505
164 gaa tct gta gct tcg ttg aaa gag agg cgc gtt gga gtc gct ggt gag   1587
165 Glu Ser Val Ala Ser Leu Lys Glu Arg Arg Val Gly Val Ala Gly Glu
166         510                 515                 520
168 cag ggt gag aag ata act ggt cta aat tcg gaa ttg gaa gat gtt tcc   1635
169 Gln Gly Glu Lys Ile Thr Gly Leu Asn Ser Glu Leu Glu Asp Val Ser
170         525                 530                 535
172 tca aaa aaa tca aca ttg aag gaa act tca tcc gtt tga tatatagtct   1684
173 Ser Lys Lys Ser Thr Leu Lys Glu Thr Ser Ser Val
174 540                 545                 550
176 ccaaattcta ttgtaatgcc attttcccaa ttcaaaaaaa aaaaaaaaaa aa        1736
179 <210> SEQ ID NO: 2
180 <211> LENGTH: 551
181 <212> TYPE: PRT
182 <213> ORGANISM: Agaricus bisporus
184 <400> SEQUENCE: 2
186 Met Ala Ser Glu Arg Gln Ile Glu Glu Leu Pro Ser Tyr Lys Tyr Ala
187 1               5                   10                  15
190 Tyr Ile Leu Thr Ala Ser Ala Cys Leu Gly Ser Val Phe His Gly Trp
191             20                  25                  30
194 Asp Val Gly Leu Ile Gly Gly Ile Leu Ser Leu Arg Ser Phe Gln Glu
```

```
195           35                    40                   45
198 Tyr Leu Gly Ile Asn Thr Lys Asn Ala Val Lys Lys Ala Ile Leu Asp
199     50                    55                   60
202 Gly Asn Ile Ile Ser Val Leu Gln Ala Gly Cys Phe Phe Gly Ala Leu
203 65                    70                   75                   80
206 Gly Thr Gly Tyr Leu Ser Ser Arg Phe Gly Arg Arg Pro Cys Leu Ile
207                   85                   90                   95
210 Ala Ser Gly Ile Val Tyr Ile Thr Gly Gly Leu Leu Gln Cys Thr Val
211                   100                  105                  110
214 Gly Leu Gly Pro Ser Gln Ala Ala Ala Leu His Val Phe Tyr Ile Gly
215           115                  120                  125
218 Arg Phe Ile Ser Gly Ile Gly Val Gly Met Val Ser Thr Leu Val Pro
219     130                   135                  140
222 Leu Tyr Ile Ser Glu Cys Val Pro Arg Thr Ile Arg Gly Arg Cys Thr
223 145                   150                  155                  160
226 Gly Thr Leu Gln Phe Ala Thr Asn Ser Gly Leu Met Leu Gly Phe Trp
227                   165                  170                  175
230 Val Asn Tyr Ser Val Ser Lys Asn Val Pro Phe Gly Glu Met Gln Trp
231                   180                  185                  190
234 Arg Ile Pro Leu Ile Ile Gln Met Ile Pro Ser Leu Leu Phe Ile Ile
235     195                   200                  205
238 Ala Met Phe Phe Gln Pro Glu Ser Pro Arg Trp Leu Val Glu His Gly
239     210                   215                  220
242 Lys His Lys Glu Ala Ala Thr Val Leu Ala Arg Thr Gly Gly Lys Asp
243 225                   230                  235                  240
246 Val Asp His Pro Ser Val Val Gln Thr Leu Glu Glu Ile Lys Gln Glu
247                   245                  250                  255
250 Phe Val Ala Ser Lys Gln Pro Ser Phe Leu Lys Gln Ile Arg Leu Val
251                   260                  265                  270
254 Gly Glu Ser Arg Ala Val Ala Leu Arg Cys Phe Ile Pro Pro Leu Val
255           275                  280                  285
258 Met Phe Phe Gln Gln Trp Thr Gly Thr Asn Ala Ile Asn Leu Tyr Ser
259     290                   295                  300
262 Pro Glu Val Phe Arg His Leu Gly Ile His Gly Thr Ser Gly Ala Leu
263 305                   310                  315                  320
266 Phe Ala Thr Gly Val Tyr Gly Val Val Lys Val Val Ser Val Ala Leu
267                   325                  330                  335
270 Ala Leu Thr Phe Ala Val Glu Arg Phe Gly Arg Lys Arg Gly Leu Ile
271                   340                  345                  350
274 Phe Gly Gly Ile Gly Gln Ala Leu Met Met Phe Trp Leu Gly Gly Tyr
275           355                  360                  365
278 Ser Ala Thr His Gln Asp Gly Thr Val Ser Pro Ala Ser His Val Ser
279     370                   375                  380
282 Ile Val Ala Leu Tyr Leu Tyr Gly Ala Phe Phe Ser Met Gly Trp Gly
283 385                   390                  395                  400
286 Pro Leu Pro Trp Val Val Ala Gly Glu Val Ala Pro Asn His Val Arg
287                   405                  410                  415
290 Ser Phe Ala Leu Ser Ile Ala Val Gly Thr His Trp Leu Phe Gly Phe
291           420                  425                  430
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PATENT APPLICATION:· US/10/533,361   TIME: 08:02:34

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294 Val Ile Ser Lys Val Thr Pro Ile Met Leu Asp Arg Ile Lys Tyr Gly
295         435                 440                 445
298 Thr Phe Leu Leu Phe Gly Phe Cys Cys Met Ile Val Ala Thr Trp Ala
299     450                 455                 460
302 Tyr Phe Cys Leu Pro Glu Thr Ser Gly Phe Ala Leu Glu Asp Ile Lys
303 465                 470                 475                 480
306 Tyr Leu Phe Glu Arg Asp Val Ile Ile Arg Ser Leu Gln Asp Ala Pro .
307             485         -       490                 495
310 Gly Gly Lys Ile Phe Leu Gly Gly Arg Arg Val Glu Ser Val Ala Ser
311         500                 505                 510
314 Leu Lys Glu Arg Arg Val Gly Val Ala Gly Glu Gln Gly Glu Lys Ile
315     515                 520                 525
318 Thr Gly Leu Asn Ser Glu Leu Glu Asp Val Ser Ser Lys Lys Ser Thr
319     530                 535                 540
322 Leu Lys Glu Thr Ser Ser Val
323 545                 550
326 <210> SEQ ID NO: 3
327 <211> LENGTH: 3638
328 <212> TYPE: DNA
329 <213> ORGANISM: Agaricus bisporus
331 <220> FEATURE:
332 <221> NAME/KEY: misc_feature
333 <222> LOCATION: (3)..(3)
334 <223> OTHER INFORMATION: n is an unknown nucleotide
337 <220> FEATURE:
338 <221> NAME/KEY: misc_feature
339 <222> LOCATION: (14)..(14)
340 <223> OTHER INFORMATION: n is an unknown nucleotide
343 <220> FEATURE:
344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: (510)..(510)
346 <223> OTHER INFORMATION: n is an unknown nucleotide
349 <400> SEQUENCE: 3
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W--> 350 gtncgatggg ttcntctggg ttaagttgca cgacgctttc ctttttcttt tatggcctgt    60
     352 ctgccctttt aacgctttat ctttcggcag ccatggatgt ccttcgtcac cgtattatca   120
     354 ctcttaatcg tggtggtgag cacatggaaa ggttcattat cgtcatccca tgacgcggtg '  180
     356 caaaattcgt cattcagagt ggaaccgata ctaggagagg attttgaaaa ggctatcgta   240
     358 tcttccgatc cattcactcc aacgacatct atatcgggtt ctcaagctac gataaccgtt   300
     360 cctcacgcat cacattcttc tctgattgta atgaccgaag accgcggttc cacccctaat   360
     362 attcgaagag cttgttgcca atgtcaaaaa aggctttt gg gcaaaccggg atggcttatc   420
     364 gagcctccag ccccagcagc taacatcggg cagagaagga aaattcatcg ggcggttgaa   480
     366 ttatcaccgt ttggttcctg agtcatctgn ragatgtacg cagatggtga taccgtgttt   540
     368 gattggcgcc gttggagaag aactatatta ttcgatggat tttttgttcg agtttgacac   600
     370 agagacagag atgatagagg tttgctattg atgtagcaaa ggatcatttg acgatggcgc   660
     372 ataggcgat ggttatcttt atgtctggaa ttataatatg tattgttccc cacttttctt   720
     374 ttatatttat taatactaat tggaagtttc agttgttgga tgagcaaagt tggtgcagat   780
     376 agaaactaga attcggattc ccatatctga ggtacctttt ccttccgctg gcaatcctgg   840
     378 ccacttcgac gtggtgacgc agagggcgcg tgctattgtt agcacatgcc atawggatcg   900
     380 acgttgcctc tcgtacttcg cgcctaggct cgctcatgcc tcgatgcatc ttttcaattc   960
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/12/2005
PATENT APPLICATION: US/10/533,361   TIME: 08:02:35

Input Set : **A:\44-05sequence listing.txt**
Output Set: **N:\CRF4\05122005\J533361.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,14,510
Seq#:4; N Pos. 495
Seq#:8; N Pos. 2774
Seq#:10; N Pos. 1262
Seq#:37; N Pos. 290,498,589

VERIFICATION SUMMARY　　　　　　　　DATE: 05/12/2005
PATENT APPLICATION:　**US/10/533,361**　　TIME: 08:02:35

Input Set : **A:\44-05sequence listing.txt**
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```
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:32
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:480
L:564 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:561
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:2760
L:853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:1260
L:984 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:975
L:990 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:981
L:990 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:987
L:1021 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1018
L:1328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:240
M:341 Repeated in SeqNo=37
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